

SEQUENCE LISTING

<110> Presnell, Scott R.
Taft, David W.

<120> A New Member of the Human
Syntaxin/Epimorphin Family

<130> 98-69

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1274

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (189)...(1049)

<400> 1

gcggccgcgg	cggcgcggag	ctcgggcggc	cgtggaggaa	ctcagcctcg	gccgcaggag	60
gcgccgggag	cggagccgcc	gggagtcgcg	caacagggtt	ccttctccat	cgtgcgccc	120
acaggggacg	cgcgccctgc	cgggagaggg	gcttctcggt	tcgcactctc	gctcccagtc	180
caggcaaa	atg aaa gac	cgg cta gca	gaa ctt ctg	gac ttg tcc	aag caa	230
	Met Lys Asp Arg	Leu Ala Glu	Leu Leu Asp	Leu Ser Lys	Gln	
	1	5	10			

tat gac cag	cag ttc cca	gac ggg gac	gat gag ttt	gac tcg ccc	cac	278
Tyr Asp Gln	Gln Phe Pro	Asp Gly Asp	Asp Glu Phe	Asp Ser Pro	His	
15	20	25	30			

gag gac atc	gtg ttc gag	acg gac cac	atc ctg gag	tcc ctg tac	cga	326
Glu Asp Ile	Val Phe Glu	Thr Asp His	Ile Leu Glu	Ser Leu Tyr	Arg	
	35	40	45			

gac atc cgg	gac att cag	gat gaa aac	cag ctg ctg	gtg gcc gac	gtg	374
Asp Ile Arg	Asp Ile Gln	Asp Glu Asn	Gln Leu Leu	Val Ala Asp	Val	
	50	55	60			

aag cgg ctg	gga aag cag	aac gcc cgc	ttc ctc acg	tcc atg cgg	cgc	422
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Lys	Arg	Leu	Gly	Lys	Gln	Asn	Ala	Arg	Phe	Leu	Thr	Ser	Met	Arg	Arg		
		65					70					75					
ctc	agc	agc	atc	aag	cgc	gac	acc	aac	tcc	atc	gcc	aag	gcc	atc	aag		470
Leu	Ser	Ser	Ile	Lys	Arg	Asp	Thr	Asn	Ser	Ile	Ala	Lys	Ala	Ile	Lys		
	80					85					90						
gcc	cgg	ggc	gag	gtc	atc	cac	tgc	aag	ctg	cgc	gcc	atg	aag	gag	ctg		518
Ala	Arg	Gly	Glu	Val	Ile	His	Cys	Lys	Leu	Arg	Ala	Met	Lys	Glu	Leu		
	95				100					105					110		
agc	gag	gcg	gct	gag	gcc	cag	cac	ggc	ccg	cac	tcg	gca	gtg	gcg	cgc		566
Ser	Glu	Ala	Ala	Glu	Ala	Gln	His	Gly	Pro	His	Ser	Ala	Val	Ala	Arg		
				115					120					125			
att	tcg	cgg	gcg	cag	tac	aac	gcg	ctc	acc	ctc	acc	ttc	cag	cgc	gcc		614
Ile	Ser	Arg	Ala	Gln	Tyr	Asn	Ala	Leu	Thr	Leu	Thr	Phe	Gln	Arg	Ala		
			130					135					140				
atg	cac	gac	tac	aac	cag	gcc	gag	atg	aag	cag	cgc	gac	aac	tgc	aag		662
Met	His	Asp	Tyr	Asn	Gln	Ala	Glu	Met	Lys	Gln	Arg	Asp	Asn	Cys	Lys		
		145				150						155					
atc	cgc	atc	cag	cgc	cag	ctg	gag	atc	atg	ggc	aag	gaa	gtc	tcg	ggc		710
Ile	Arg	Ile	Gln	Arg	Gln	Leu	Glu	Ile	Met	Gly	Lys	Glu	Val	Ser	Gly		
	160					165					170						
gac	cag	atc	gag	gac	atg	ttc	gag	cag	ggc	aag	tgg	gac	gtg	ttt	tcc		758
Asp	Gln	Ile	Glu	Asp	Met	Phe	Glu	Gln	Gly	Lys	Trp	Asp	Val	Phe	Ser		
	175				180					185					190		
gag	aac	ttg	ctg	gcc	gac	gtg	aag	ggc	gcg	cgg	gcc	gcc	ctc	aac	gag		806
Glu	Asn	Leu	Leu	Ala	Asp	Val	Lys	Gly	Ala	Arg	Ala	Ala	Leu	Asn	Glu		
				195					200					205			
atc	gag	agc	cgc	cac	cgc	gaa	ctg	ctg	cgc	ctg	gag	agc	cgc	atc	cgc		854
Ile	Glu	Ser	Arg	His	Arg	Glu	Leu	Leu	Arg	Leu	Glu	Ser	Arg	Ile	Arg		
		210					215					220					
gac	gta	cac	gag	ctc	ttc	ttg	cag	atg	gcg	gtg	ctg	gtg	gag	aag	cag		902
Asp	Val	His	Glu	Leu	Phe	Leu	Gln	Met	Ala	Val	Leu	Val	Glu	Lys	Gln		
		225					230					235					
gcc	gac	acc	ctg	aac	gtc	atc	gag	ctc	aac	gta	caa	aag	acg	gtc	gac		950

Ala Asp Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp
 240 245 250

tac acc ggc cag gcc aag gcg cag gtg cgg aag gcc gtg cag tac gag 998
 Tyr Thr Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu
 255 260 265 270

gag aag aac ccc tgc cgg acc ctc tgc tgc ttc tgc tgt ccc tgc ctc 1046
 Glu Lys Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu
 275 280 285

aag tagcaggccg gcccgggccg ccaccgccc tcccagacca tggagcgcgc 1099
 tgggaaggac gcaccaaagc cgggagctct gccctgcagg gagttgcccc aaccctttcc 1159
 ggaactcagt ctttagaaaa gaaacgccag gttcaagaat tgcaaaccag cctgtgcttg 1219
 gaaagatggg tagttgatac cgtccgatga ttcttcagta aagatagatt cccac 1274

<210> 2

<211> 287

<212> PRT

<213> Homo sapiens

<400> 2

Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15
 Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30
 Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45
 Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
 50 55 60
 Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80
 Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
 85 90 95
 Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110
 Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
 115 120 125
 Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140
 Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160
 Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190
 Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205
 Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
 210 215 220
 His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240
 Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255
 Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270
 Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
 275 280 285

<210> 3

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> variation

<222> (1)...(861)

<223> N is any nucleotide.

<400> 3

atgaargaym gnytnngnga rytnytngay ytnwsnaarc artaygayca rcarttyccn	60
gayggngayg aygarttyga ywsnccncay gargayathg tnttygarac ngaycayath	120
ytngarwsny tntaymgnga yathmgngay athcargayg araaycaryt nytngtngcn	180
gaygtnaarm gnytnngnaa rcaraaygcn mgnttyytna cnwsnatgmg nmgnytnwsn	240
wsnathaarm gngayacnaa ywsnathgcn aargcnatha argcnmgngg ngargtnath	300
caytgyaary tnmngngcnat gaargarytn wsngargcng cngargcnca rcayggncn	360
caywsngcng tngcnmgngat hwsnmngncn cartayaayg cnytnacnyt nacnttycar	420
mgngcnatgc aygaytayaa ycargcngar atgaarcarm gngayaaytg yaarathmgn	480
athcarmgnc arytnгарat hatgggnaar gargtnwsng gngaycarat hgargayatg	540
tytgarcarg gnaartggga ygtnttywsn garaayytny tngcngaygt naarggngcn	600
mgngcngcny tnaaygarat hgarwsnmgn caymgngary tnytnmgnyt ngarwsnmgn	660
athmgngayg tncaygaryt nttyytnкар atggcngtny tngtngaraa rcargcngay	720
acnytnaayg tnathgaryt naaygtncar aaracngtny aytayacngg ncargcnaar	780
gcncargtnm gnaargcngt ncartaygar garaaraayc cntgymgnac nytntgytgy	840
ttytgytgyc cntgyytnaa r	861

<210> 4
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 4
 tggcggtgct ggtggaga 18

<210> 5
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 5
 ccggcagggg ttcttctc 18

<210> 6
 <211> 287
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15
 Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30
 Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45
 Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asn Val Lys Arg
 50 55 60
 Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80
 Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Pro
 85 90 95
 Pro Glu Val Ile His Cys Asn Val Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110
 Ala Ala Glu Ala Gln His Gly Pro Ala Leu Gly Ser Gly Gly Ile Ser
 115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140
 Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160
 Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175
 Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190
 Leu Leu Ala Asp Val Lys Gly Val Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205
 Ser Arg His Arg Glu Leu Val Arg Leu Glu Ser Ala Ile Arg Asp Val
 210 215 220
 His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240
 Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255
 Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270
 Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
 275 280 285

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 7
 ggacgtgttt tccgagaact tg 22

<210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 8
 cgaccgtctt ttgtacgttg ag 22

<210> 9
 <211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 9

Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
1					5				10					15	

Gly
 Gly
 Ser
 Gly
 Gly
 Ser
 Gly
 Gly
 Gly
 Gly
 Ser
 Gly
 Gly
 Gly
 Gly
 Ser